SEQUENCE LISTING

<110> MIYAGAWA, SHUJI
OKABE, MASARU

<120> MODIFIED CRE RECOMBINASE GENE FOR MAMMALS

<130> 197330US0

<140> 09/662,128
<141> 2000-09-14

<150> JP11-264364
<151> 1999-09-17

<160> 6

<170> PatentIn version 3.0

<210> 1
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1050)

B'

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: synthetic dna

<400> 1

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atg ccc aag aag aag agg aag gtg agc aac ctg ctg acc gtg cac cag       48
Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
1               5                   10                  15

aac ctg ccc gcc ctg ccc gtg gac gcc acc agc gac gag gtg cgc aag       96
Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
            20                  25                  30

aac ctg atg gac atg ttc cgc gac cgc cag gcc ttc agc gag cac acc      144
Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
        35                  40                  45

tgg aag atg ctg ctg agc gtg tgc cgc agc tgg gcc gcc tgg tgc aag      192
Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
    50                  55                  60

ctg aac aac cgc aag tgg ttc ccc gcc gag ccc gag gac gtg cgc gac      240
Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
65                  70                  75                  80

tac ctg ctg tac ctg cag gcc cgc ggc ctg gcc gtg aag acc atc cag      288
Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
```

```
                85                  90                  95

cag cac ctg ggc cag ctg aac atg ctg cac cgc cgc agc ggc ctg ccc      336
Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
            100                 105                 110

cgc ccc agc gac agc aac gcc gtg agc ctg gtg atg cgc cgc atc cgc      384
Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
        115                 120                 125

aag gag aac gtg gac gcc ggc gag cgc gcc aag cag gcc ctg gcc ttc      432
Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
    130                 135                 140

gag cgc acc gac ttc gac cag gtg cgc agc ctg atg gag aac agc gac      480
Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
145                 150                 155                 160

cgc tgc cag gac atc cgc aac ctg gcc ttc ctg ggc atc gcc tac aac      528
Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
                165                 170                 175

acc ctg ctg cgc atc gcc gag atc gcc cgc atc cgc gtg aag gac atc      576
Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
            180                 185                 190

agc cgc acc gac ggc ggc cgc atg ctg atc cac atc ggc cgc acc aag      624
Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
        195                 200                 205

acc ctg gtg agc acc gcc ggc gtg gag aag gcc ctg agc ctg ggc gtg      672
Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
    210                 215                 220

acc aag ctg gtg gag cgc tgg atc agc gtg agc ggc gtg gcc gac gac      720
Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
225                 230                 235                 240

ccc aac aac tac ctg ttc tgc cgc gtg cgc aag aac ggc gtg gcc gcc      768
Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
                245                 250                 255

ccc agc gcc acc agc cag ctg agc acc cgg gcc ctg gag ggc atc ttc      816
Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
            260                 265                 270

gag gcc acc cac cgc ctg atc tac ggc gcc aag gac gac agc ggc cag      864
Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
        275                 280                 285

cgc tac ctg gcc tgg agc ggc cac agc gcc cgc gtg ggc gcc gcc cgc      912
Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
    290                 295                 300

gac atg gcc cgc gcc ggc gtg agc atc ccc gag atc atg cag gcc ggc      960
Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
305                 310                 315                 320
```

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ggc tgg acc aac gtg aac atc gtg atg aac tac atc cgc aac ctg gac      1008
Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
                325                 330                 335

agc gag acc ggc gcc atg gtg cgc ctg ctg gag gac ggc gac            1050
Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
            340                 345                 350
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<210> 2
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<212> PRT
<213> Artificial Sequence

<220>
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<222> ()..()
<223> Description of Artificial Sequence: synthetic peptide

<400> 2

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Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
1               5                   10                  15

Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
            20                  25                  30

Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
        35                  40                  45

Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
    50                  55                  60

Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
65                  70                  75                  80

Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
                85                  90                  95

Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
            100                 105                 110

Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
        115                 120                 125

Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
    130                 135                 140
```

Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
145 150 155 160

Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
165 170 175

Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
180 185 190

Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
195 200 205

Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
210 215 220

Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
225 230 235 240

Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
245 250 255

Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
260 265 270

Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
275 280 285

Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
290 295 300

Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
305 310 315 320

Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
325 330 335

Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
340 345 350

<210> 3
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: synthetic DNA

<400> 3
ataacttcgt atagcataca ttatacgaag ttat 34

<210> 4
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: synthetic DNA

<400> 4
ttcgtatagc atagattata cgaagttat 29

b' cncl.

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: synthetic DNA

<400> 5
ataacttcgt atagcataca ttatacgaa 29

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: synthetic DNA

<400> 6
cccaagaaga agaggaaggt g 21